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UniProtKB/Swiss-Prot entry

P07118

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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

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Entry information

Entry name **SYV_ECOLI**
 Primary accession number **P07118**
 Secondary accession numbers **P78142 Q2M651 Q7X4V7**
 Integrated into Swiss-Prot on **April 1, 1988**
 Sequence was last modified on **November 1, 1997 (Sequence version 2)**
 Annotations were last modified on **April 8, 2008 (Entry version 83)**

Name and origin of the protein

Protein name **Valyl-tRNA synthetase**
 Synonyms **EC 6.1.1.9**
Valine--tRNA ligase
ValRS

Gene name

Name: valS

OrderedLocusNames: **b4258, JW4215**

From

Escherichia coli (strain K12) [TaxID: 83333] [HAMAP proteome]

Taxonomy

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales
Enterobacteriaceae; Escherichia.

Protein existence

1: Evidence at protein level;

References

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].

STRAIN=K12;

DOI=10.1093/nar/15.21.9081; PubMed=3317277 [NCBI, ExPASy, EBI, Israel, Japan]

Haertlein M., Frank R., Madern D.;

"Nucleotide sequence of Escherichia coli valyl-tRNA synthetase gene valS.";

Nucleic Acids Res. 15:9081-9082(1987).

[2]

NUCLEOTIDE SEQUENCE [GENOMIC DNA].

STRAIN=K12;

PubMed=3275660 [NCBI, ExPASy, EBI, Israel, Japan]

Heck J.D., Hatfield G.W.;

"Valyl-tRNA synthetase gene of Escherichia coli K12. Primary structure and homology within a fami

of aminoacyl-tRNA synthetases.";

J. Biol. Chem. 263:868-877(1988).

[3] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=K12 / MG1655 / ATCC 47076;

DOI=10.1093/nar/23.12.2105; PubMed=7610040 [NCBI, ExPASy, EBI, Israel, Japan]

Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L., Blattner F.R.;

"Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes.";

Nucleic Acids Res. 23:2105-2119(1995).

[4] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=K12 / MG1655 / ATCC 47076;

DOI=10.1126/science.277.5331.1453; PubMed=9278503 [NCBI, ExPASy, EBI, Israel, Japan]

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

"The complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).

[5] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=K12 / W3110 / ATCC 27325 / DSM 5911;

DOI=10.1038/msb4100049; PubMed=16738553 [NCBI, ExPASy, EBI, Israel, Japan]

Hayashi K., Morooka N., Yamamoto Y., Fujita K., Isono K., Choi S., Ohtsubo E., Baba T., Wanner B.L., Mori H., Horiuchi T.;

"Highly accurate genome sequences of Escherichia coli K-12 strains MG1655 and W3110.";

Mol. Syst. Biol. 2:E1-E5(2006).

[6] NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-801.

STRAIN=B / MD6014;

Ramchandani J.H., Bhattacharjee S.K., Mahajan S.K.;

"Nucleotide sequence of the valS-holC region of Escherichia coli B.";

Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

[7] PROTEIN SEQUENCE OF 1-12.

STRAIN=K12 / EMG2;

PubMed=9298646 [NCBI, ExPASy, EBI, Israel, Japan]

Link A.J., Robison K., Church G.M.;

"Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12.";

Electrophoresis 18:1259-1313(1997).

[8] MUTAGENESIS OF THR-222.

DOI=10.1126/science.1057718; PubMed=11313495 [NCBI, ExPASy, EBI, Israel, Japan]

Doering V., Mootz H.D., Nangle L.A., Hendrickson T.L., de Crecy-Lagard V., Schimmel P., Marliere P.;

"Enlarging the amino acid set of Escherichia coli by infiltration of the valine coding pathway.";

Science 292:501-504(2001).

[9] KINETIC PARAMETERS, AND MUTAGENESIS OF LYS-277.

DOI=10.1021/bi0205101; PubMed=12475234 [NCBI, ExPASy, EBI, Israel, Japan]

Hountondji C., Lazennec C., Beauvallet C., Dessen P., Pernollet J.-C., Plateau P., Blanquet S.;

"Crucial role of conserved lysine 277 in the fidelity of tRNA aminoacylation by Escherichia coli valyl-tRNA synthetase.";

Biochemistry 41:14856-14865(2002).

Comments

- **FUNCTION:** Catalyzes the attachment of valine to tRNA(Val). As ValRS can inadvertently accommodate and process structurally similar amino acids such as threonine, to avoid such error it has a "posttransfer" editing activity that hydrolyzes mischarged Thr-tRNA(Val) in a tRNA-dependent manner.
- **CATALYTIC ACTIVITY:** ATP + L-valine + tRNA(Val) = AMP + diphosphate + L-valyl-tRNA(Val).

- **BIOPHYSICOCHEMICAL PROPERTIES:**

Kinetic parameters: $K_M=0.1 \mu\text{M}$ for tRNA;

$K_M=47 \mu\text{M}$ for valine;

- **SUBUNIT:** Monomer.

- **INTERACTION:**

P46837:yhgF; NbExp=1; IntAct=EBI-559242, EBI-554743;

- **SUBCELLULAR LOCATION:** Cytoplasm.

- **DOMAIN:** ValRS has two distinct active sites: one for aminoacylation and one for editing. The misactivated threonine is translocated from the active site to the editing site.

- **DOMAIN:** The C-terminal coiled-coil domain is crucial for aminoacylation activity (*By similarity*).

- **SIMILARITY:** Belongs to the class-I aminoacyl-tRNA synthetase family. ValS type 1 subfamily [view classification].

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Cross-references

Sequence databases

	X05891; CAA29322.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	J03497; AAA24657.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	U14003; AAA97155.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
EMBL	U00096; AAC77215.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AP009048; BAE78255.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AY283771; AAP43521.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	E65238; SYECVT.	
RefSeq	AP_004754.1; -. NP_418679.1; -.	

3D structure databases

HSSP P96142; 1IVS. [HSSP ENTRY / PDB]

ModBase P07118.

Protein-protein interaction databases

DIP DIP:11112N; -.

IntAct P07118; -.

Enzyme and pathway databases

BioCyc EcoCyc:VALS-MON; -.

2D gel databases

ECO2DBASE E106.0; 6TH EDITION.

Organism-specific databases

EchoBASE EB1060; -.

EcoGene EG11067; valS.

Ontologies

GO GO:0005515; Molecular function: protein binding (*inferred from physical interaction from IntAct*).

GO QuickGo
view.

Family and domain databases

UniProtKB/Swiss-Prot entry P07118 [SYV_ECOLI] Valyl-tRNA synthetase

HAMAP MF_02004; -, 1.
PBIL [Family / Alignment / Tree]
 IPR001412; aa-tRNA-synth_I_CS.
 IPR002300; aa-tRNA-synth_Ia.
InterPro IPR014729; Rossmann-like_a/b/a_fold.
 IPR013155; V/L/I-tRNA-synth_anticodon-bd.
 IPR002303; Val-tRNA_synth_Ia.
 Graphical view of domain structure.
Gene3D G3DSA:3.40.50.620; Rossmann-like_a/b/a_fold; 1.
PANTHER PTHR11946:SF5; tRNA-synt_val; 1.
Pfam PF08264; Anticodon_1; 1.
 PF00133; tRNA-synt_1; 1.
 Pfam graphical view of domain structure.
PRINTS PR00986; TRNASYNTHVAL.
TIGRFAMs TIGR00422; valS; 1.
PROSITE PS00178; AA_TRNA_LIGASE_I; 1.
BLOCKS P07118.
Genome annotation databases
GeneID 948785; -.
GenomeReviews U00096_GR; b4258.
 AP009048_GR; JW4215.
KEGG ecj:JW4215; -.
 eco:b4258; -.
CMR P07118; b4258.
Other
ProtoNet P07118.
UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Aminoacyl-tRNA synthetase; ATP-binding; Coiled coil; Complete proteome; Cytoplasm; Direct protein sequencing; Ligase; Nucleotide-binding; Protein biosynthesis.

Features

Feature table viewer



Feature aligner

Key	From	To	Length	Description
CHAIN	1	951	951	Valyl-tRNA synthetase.
COILED	880	944	65	Potential.
MOTIF	42	52	11	"HIGH" region.
MOTIF	554	558	5	"KMSKS" region.
BINDING	557	557		ATP (By similarity).
MUTAGEN	222	222		T->P: Produces mischarged Thr-tRNA(Val) and Cys-tRNA(Val).
MUTAGEN	277	277		K->A: Reduces posttransfer Thr-tRNA(Val) editing rate significantly and alters amino acid discrimination in the editing site, resulting in hydrolysis of the correctly charged cognate product.
CONFLICT	107	107		R -> A (in Ref. 2; AAA24657).
CONFLICT	148	148		G -> D (in Ref. 6; AAP43521).
CONFLICT	452	452		D -> E (in Ref. 6; AAP43521).
CONFLICT	465	465		V -> A (in Ref. 6; AAP43521).
CONFLICT	694	694		S -> T (in Ref. 1; CAA29322).

FTId

PRO_000010621

UniProtKB/Swiss-Prot entry P07118 [SYV_ECOLI] Valyl-tRNA synthetase

1 460 5 500 10

CONFLICT 833 833 A -> R (in Ref. 2; AAA24657).

Sequence information

Length: 951 AA [This is the length of the unprocessed precursor]

Molecular weight: 108192 Da [This is the MW of the unprocessed precursor]

CRC64: 3FBE09CF1E7D40BC [This is a checksum on the sequence]

10	20	30	40	50	60
MEKTYNPQDI	EQPLYEHWEK	QGYFKPNGDE	SQESFCIMIP	PPNVTGSLHM	GHAFAQOTIMD
70	80	90	100	110	120
TMIRYQRMQG	KNTLWQVGTD	HAGIATQMVV	ERKIAAEEGK	TRHDYGREAF	IDKIWEWKAE
130	140	150	160	170	180
SGGTITRQMR	RLGNSVDWER	ERFTMDEGLS	NAVKEVFVRL	YKEDLIYRGK	RLVNWDPKLR
190	200	210	220	230	240
TAISDLEVEN	RESKGSMDWHI	RYPLADGAKT	ADGKDYLVA	TTRPETLLGD	TGVAVNPEDP
250	260	270	280	290	300
RYKDLIGKYV	ILPLVNRRI	IVGDEHADME	KGTGCVKITP	AHDFNDYEVG	KRHALPMINI
310	320	330	340	350	360
LTFDGDIRE	AQVFDTKGNE	SDVYSSEIPA	EFQKLERFAA	RKAVVAAVDA	LGLLEEIKPH
370	380	390	400	410	420
DLTVFYGDRG	GVVIEPMLTD	QWYVRADVLA	KPAVEAVENG	DIQFVVPKQYE	NMYFSWMRDI
430	440	450	460	470	480
QDWCISRQLW	WGHRIPAWYD	EAGNVYVGRN	EDEVKRNENL	GADVVLRLQDE	DVLDTWFSSA
490	500	510	520	530	540
LWTFSTLGWP	ENTDALRQFH	PTSVMVSGFD	IIFFWIARMI	MMTMHFIDE	NGKPQVPFHT
550	560	570	580	590	600
VYMTGLIRDD	EGQKMSKSKG	NVIDPLDMVD	GISLPELLEK	RTGNMMQPQL	ADKIRKRTK
610	620	630	640	650	660
QFPNGIEPHG	TDALRFTLAA	LASTGRDINW	DMKRLEGYRN	FCNKLWNASR	FVLMNTEGQD
670	680	690	700	710	720
CGFNGGEMTL	SLADRWILAE	FNQTIKAYRE	ALDSFRFDIA	AGILYEFTWN	QFCDWYLELT
730	740	750	760	770	780
KPVMNGGTEA	ELRGTRHTLV	TVLEGLLRLA	HPIIPFITET	IWQRVKVLG	ITADTIMLQP
790	800	810	820	830	840
FPQYDASQVD	EAALADTEWL	KQAIVAVRNI	RAEMNIAPGK	PLELLLRGCS	ADAERRNVEN
850	860	870	880	890	900
RGFLQTLARL	ESITVLPADD	KGPVSVTKII	DGAELLIPMA	GLINKEDELA	RLAKEVAKIE
910	920	930	940	950	
GEISRIENKL	ANEGFVARAP	EAVIAKEREK	LEGYAEAKAK	LIEQQAVIAA	L

P07118 in
FASTA
format

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BLAST BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-
MODEL



NPSA Sequence analysis
tools



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NiceBlast

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

Program: NCBI BLASTP 2.2.17 [Aug-26-2007]
Databases: UniProtKB Fungi 358,091 sequences; 157,054,478 total letters
Query: 951 Amino acids Date run: 2008-04-17 14:16:56 UTC+0100

Taxonomic view

HTML view

Printable view

Hit *BLAST* to perform a BLAST search of one of the results with the same parameters

Send selected sequences to Clustal W (multiple alignment)

Soumettre la requête

Select up to...

☐ Include query sequence

Score	E-value	Accession number	Entry name	Database	Length
		A5DX19	BLAST A5DX19_LODEL	tr	1103 Amino acids
<input type="checkbox"/> 699	0.0	Valyl-tRNA synthetase, mitochondrial [Gene: LELG_01906] - <i>Lodderomyces elongisporus</i> (Yeast) (<i>Saccharomyces elongisporus</i>).			
		Q59JY3	BLAST Q59JY3_CANAL	tr	1119 Amino acids
<input type="checkbox"/> 696	0.0	Probable valyl-tRNA synthetase [Gene: VAS1 OR CaO19.8875] - <i>Candida albicans</i> (Yeast).			
		Q59JY1	BLAST Q59JY1_CANAL	tr	1119 Amino acids
<input type="checkbox"/> 693	0.0	Probable valyl-tRNA synthetase [Gene: VAS1 OR CaO19.1295] - <i>Candida albicans</i> (Yeast).			

<input type="checkbox"/>	692	0.0	Q75EP5	BLAST	Q75EP5_ASHGO	tr	1098 Amino acids
			AAR034Wp [Gene: AAR034W OR AGOS_AAR034W] - <i>Ashbya gossypii</i> (Yeast) (<i>Eremothecium gossypii</i>).				
<input type="checkbox"/>	689	0.0	A7TDX6	BLAST	A7TDX6_VANPO	tr	1124 Amino acids
			Putative uncharacterized protein [Gene: Kpol_1018p134] - <i>Vanderwaltozyma polyspora</i> (strain ATCC 22028 / DSM 70294) (<i>Kluyveromyces polysporus</i>).				
<input type="checkbox"/>	688	0.0	Q4P8Q1	BLAST	Q4P8Q1_USTMA	tr	1240 Amino acids
			Putative uncharacterized protein [Gene: UM03512.1] - <i>Ustilago maydis</i> (<i>Smut fungus</i>).				
<input type="checkbox"/>	682	0.0	Q6BUV3	BLAST	Q6BUV3_DEBHA	tr	1054 Amino acids
			Similar to sp P07806 <i>Saccharomyces cerevisiae</i> YGR094w VAS1 valyl-tRNA synthetase [Gene: DEHA0C08525g] - <i>Debaryomyces hansenii</i> (Yeast) (<i>Torulasporea hansenii</i>).				
<input type="checkbox"/>	682	0.0	A5DLH6	BLAST	A5DLH6_PICGU	tr	1065 Amino acids
			Putative uncharacterized protein [Gene: PGUG_04127] - <i>Pichia guilliermondii</i> (Yeast) (<i>Candida guilliermondii</i>).				
<input type="checkbox"/>	681	0.0	Q6FTE7	BLAST	Q6FTE7_CANGA	tr	1105 Amino acids
			Similar to sp P07806 <i>Saccharomyces cerevisiae</i> YGR094w VAS1 valyl-tRNA synthetase [Gene: CAGL0G03091g] - <i>Candida glabrata</i> (Yeast) (<i>Torulopsis glabrata</i>).				
<input type="checkbox"/>	679	0.0	P28350	BLAST	SYV_NEUCR	sp	1093 Amino acids
			Valyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.9) (Valine-tRNA ligase) (ValRS) [Gene: cyt-20 OR un-3 OR NCU01965] - <i>Neurospora crassa</i> .				
<input type="checkbox"/>	679	0.0	P28350-2	BLAST	SYV_NEUCR	sp_vs	1050 Amino acids
			Isoform Cytoplasmic of P28350 - <i>Neurospora</i> Valyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.9) (Valine-tRNA ligase) (ValRS) [Gene: cyt-20 OR un-3 OR NCU01965] - <i>Neurospora crassa</i> .				
<input type="checkbox"/>	676	0.0	A3LVX8	BLAST	A3LVX8_PICST	tr	1051 Amino acids
			Valyl-tRNA synthetase (EC 6.1.1.9) [Gene: VAS1 OR PICST_72245] - <i>Pichia stipitis</i> (Yeast).				
<input type="checkbox"/>	676	0.0	Q2URW3	BLAST	Q2URW3_ASPOR	tr	1078 Amino acids
			Valyl-tRNA synthetase [Gene: AO090005000667] - <i>Aspergillus oryzae</i> .				

<input type="checkbox"/>	675	0.0	A8Q4A4	BLAST	A8Q4A4_9BASI	tr	1080 Amino acids
			Putative uncharacterized protein [Gene: MGL_2516] - <i>Malassezia globosa</i> CBS 7966.				
<input type="checkbox"/>	675	0.0	A1DB92	BLAST	A1DB92_NEOFI	tr	1057 Amino acids
			Valyl-tRNA synthetase [Gene: NFIA_097600] - <i>Neosartorya fischeri</i> (strain ATCC 1020 / DSM 3700 / NRRL 181) (<i>Aspergillus fischerianus</i> (strain ATCC 1020 / DSM 3700 / NRRL 181)).				
<input type="checkbox"/>	672	0.0	Q4WCD6	BLAST	Q4WCD6_ASPFU	tr	1057 Amino acids
			Valyl-tRNA synthetase (EC 6.1.1.9) [Gene: AFUA_8G04800] - <i>Aspergillus fumigatus</i> (<i>Sartorya fumigata</i>).				
<input type="checkbox"/>	672	0.0	B0Y9Y5	BLAST	B0Y9Y5_ASPFU	tr	1057 Amino acids
			Valyl-tRNA synthetase [Gene: AFUB_082710] - <i>Aspergillus fumigatus</i> A1163.				
<input type="checkbox"/>	668	0.0	A4QVP7	BLAST	A4QVP7_MAGGR	tr	1099 Amino acids
			Putative uncharacterized protein [Gene: MGG_04396] - <i>Magnaporthe grisea</i> (<i>Rice blast fungus</i>) (<i>Pyricularia grisea</i>).				
<input type="checkbox"/>	668	0.0	P07806	BLAST	SYV_YEAST	sp	1104 Amino acids
			Valyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.9) (Valine-tRNA ligase) (ValRS) [Gene: VAS1 OR YGR094W] - <i>Saccharomyces cerevisiae</i> (<i>Baker's yeast</i>).				
<input type="checkbox"/>	668	0.0	A6ZV76	BLAST	A6ZV76_YEAST	tr	1104 Amino acids
			Mitochondrial valyl-tRNA synthetase [Gene: VAS1 OR SCY_2309] - <i>Saccharomyces cerevisiae</i> (strain YJM789) (<i>Baker's yeast</i>).				
<input type="checkbox"/>	668	0.0	P07806-2	BLAST	SYV_YEAST	sp_vs	1058 Amino acids
			Isoform Cytoplasmic of P07806 - <i>Saccharomyces cerevisiae</i> (<i>Baker's Valyl-tRNA synthetase, mitochondrial precursor</i> (EC 6.1.1.9) (Valine-tRNA ligase) (ValRS) [Gene: VAS1 OR YGR094W] - <i>Saccharomyces cerevisiae</i> (<i>Baker's yeast</i>)).				
<input type="checkbox"/>	666	0.0	Q6CQR5	BLAST	Q6CQR5_KLULA	tr	1091 Amino acids
			Similar to sp P07806 <i>Saccharomyces cerevisiae</i> YGR094W VAS1 valyl-tRNA synthetase [Gene: KLLA0D14971g] - <i>Kluyveromyces fragilis</i> (<i>Yeast</i>) (<i>Candida sphaerica</i>).				
<input type="checkbox"/>	666	0.0	Q6C109	BLAST	Q6C109_YARLI	tr	1047 Amino acids

<input type="checkbox"/>			Similar to sp P07806 Saccharomyces cerevisiae YGR094w VAS1 valyl-tRNA synthetase [Gene: YALI0F20218g] - <i>Yarrowia lipolytica</i> (<i>Candida lipolytica</i>).				
<input type="checkbox"/>	661	0.0	Q1E5K2	BLAST	Q1E5K2_COCIM	tr	1045 Amino acids
<input type="checkbox"/>			Valyl-tRNA synthetase, mitochondrial [Gene: CIMG_02161] - <i>Coccidioides immitis</i> .				
<input type="checkbox"/>			O75005	BLAST	SYV_SCHPO	sp	980 Amino acids
<input type="checkbox"/>	660	0.0	Probable valyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS) [Gene: SPBC1709.02c OR SPBC1734.18c] - <i>Schizosaccharomyces pombe</i> (<i>Fission yeast</i>).				
<input type="checkbox"/>	657	0.0	A1C423	BLAST	A1C423_ASPL	tr	1057 Amino acids
<input type="checkbox"/>			Valyl-tRNA synthetase [Gene: ACLA_058200] - <i>Aspergillus clavatus</i> .				
<input type="checkbox"/>	657	0.0	A8NWU5	BLAST	A8NWU5_COPCI	tr	1078 Amino acids
<input type="checkbox"/>			Putative uncharacterized protein [Gene: CC1G_00124] - <i>Coprinopsis cinerea okayama7#130</i> .				
<input type="checkbox"/>	656	0.0	A2R8Q8	BLAST	A2R8Q8_ASPNG	tr	1054 Amino acids
<input type="checkbox"/>			Putative frameshift (EC 6.1.1.9) [Gene: An16g08020] - <i>Aspergillus niger</i> .				
<input type="checkbox"/>	652	0.0	A1CCL2	BLAST	A1CCL2_ASPL	tr	1057 Amino acids
<input type="checkbox"/>			Valyl-tRNA synthetase [Gene: ACLA_062330] - <i>Aspergillus clavatus</i> .				
<input type="checkbox"/>	647	0.0	B0DK38	BLAST	B0DK38_LACBI	tr	1039 Amino acids
<input type="checkbox"/>			Predicted protein [Gene: LACBIDRAFT_303702] - <i>Laccaria bicolor S238N-H82</i> .				
<input type="checkbox"/>	646	0.0	Q2H436	BLAST	Q2H436_CHAGB	tr	1058 Amino acids
<input type="checkbox"/>			Putative uncharacterized protein [Gene: CHGG_06579] - <i>Chaetomium globosum</i> (<i>Soil fungus</i>).				
<input type="checkbox"/>	641	0.0	Q5KMF6	BLAST	Q5KMF6_CRYNE	tr	1109 Amino acids
<input type="checkbox"/>			Valine-tRNA ligase, putative (Putative uncharacterized protein) [Gene: CNB01880 OR CNBB3840] - <i>Cryptococcus neoformans</i> (<i>Filobasidiella neoformans</i>).				
<input type="checkbox"/>	624	e-178	Q0UUP7	BLAST	Q0UUP7_PHANO	tr	1075 Amino acids
<input type="checkbox"/>			Putative uncharacterized protein [Gene: SNOG_04517] - <i>Phaeosphaeria nodorum</i> (<i>Septoria nodorum</i>).				

<input type="checkbox"/>		Q0D1T2	BLAST	Q0D1T2_ASPTN	tr	1313 Amino acids
<input type="checkbox"/>	610	e-173				
			Valyl-tRNA synthetase, mitochondrial [Gene: ATEG_00102] - <i>Aspergillus terreus</i> (strain NIH 2624).			
<input type="checkbox"/>	591	e-168	BLAST	Q5BD96_EMENI	tr	1294 Amino acids
			Putative uncharacterized protein [Gene: AN1484.2] - <i>Emicella nidulans</i> (<i>Aspergillus nidulans</i>).			
<input type="checkbox"/>	583	e-165	BLAST	Q8SS27_ENCUC	tr	921 Amino acids
			VALYL tRNA SYNTHETASE [Gene: ECU04_1140] - <i>Encephalitozoon cuniculi</i> .			
<input type="checkbox"/>	560	e-158	BLAST	A7EFY6_SCLS1	tr	1027 Amino acids
			Putative uncharacterized protein [Gene: SS1G_04227] - <i>Sclerotinia sclerotiorum</i> (strain ATCC 18683 / 1980 / Ss-1) (<i>White mold</i>) (<i>Whetzelinia sclerotiorum</i>).			
<input type="checkbox"/>	528	e-148	BLAST	Q0CDA1_ASPTN	tr	998 Amino acids
			Valyl-tRNA synthetase, mitochondrial [Gene: ATEG_08333] - <i>Aspergillus terreus</i> (strain NIH 2624).			
<input type="checkbox"/>	491	e-137	BLAST	Q5KTV8_9MICR	tr	591 Amino acids (fragment)
			Valyl tRNA synthetase - <i>Glugea plecoglossi</i> .			
<input type="checkbox"/>	476	e-133	BLAST	Q5KTV7_ENCNE	tr	600 Amino acids (fragment)
			Valyl tRNA synthetase - <i>Encephalitozoon hellem</i> .			
<input type="checkbox"/>	430	e-119	BLAST	A6RIC5_BOTFB	tr	723 Amino acids
			Putative uncharacterized protein [Gene: BC1G_00196] - <i>Botryotinia fuckeliana</i> (strain B05.10) (<i>Noble rot fungus</i>) (<i>Botrytis cinerea</i>).			
<input type="checkbox"/>	424	e-117	BLAST	O14160_SCHPO	tr	950 Amino acids
			Valine-tRNA ligase Vas1 (EC 6.1.1.9) [Gene: vas1 OR SPAC4A8.08c] - <i>Schizosaccharomyces pombe</i> (<i>Fission yeast</i>).			
<input type="checkbox"/>	375	e-103	BLAST	Q2GXV2_CHAGB	tr	980 Amino acids
			Putative uncharacterized protein [Gene: CHGG_07202] - <i>Chaetomium globosum</i> (<i>Soil fungus</i>).			
<input type="checkbox"/>	341	2e-92	BLAST	A6QZF7_AJECN	tr	614 Amino acids
			Valyl-tRNA synthetase 2 [Gene: HCAG_02764] - <i>Ajellomyces capsulata</i> (strain NAM1) (<i>Histoplasma capsulatum</i>).			